

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/976,059B
Source: JFW
Date Processed by STIC: 2-15-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

SERIAL NUMBER 09/976/059B

ERROR DETECTED

SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>..<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>..<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>..<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>..<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.

8 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>..<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>..<223> section is required when <213> response is Unknown, or is Artificial Sequence.

11 Use of <220> Sequence(s) missing the <220>..<223> section and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can only represent a single nucleotide. "Xaa" can only represent a single amino acid.



IFW16 IFV

RAW SEQUENCE LISTING

DATE: 02/15/2005

PATENT APPLICATION: US/09/976,059B

TIME: 07:48:04

Input Set : A:\3002-2US Sequ List AMENDED Dec 2004.ST25.txt

Output Set: N:\CRF4\02152005\I976059B.raw

3 <110> APPLICANT: Farnet, Chris
 4 Zazopoulos, Emmanuel
 5 Staffa, Alfredo
 7 <120> TITLE OF INVENTION: GENE CLUSTER FOR RAMOPLANIN BIOSYNTHESIS
 9 <130> FILE REFERENCE: 3002-2US
 11 <140> CURRENT APPLICATION NUMBER: US 09/976,059B
 > 12 <141> CURRENT FILING DATE: 2001-10-15
 14 <150> PRIOR APPLICATION NUMBER: US 60/239,924
 15 <151> PRIOR FILING DATE: 2000-10-13
 17 <160> NUMBER OF SEQ ID NOS: 46
 19 <170> SOFTWARE: PatentIn version 3.0

ORDERED SEQUENCES

9735 <210> SEQ ID NO: 46
 9736 <211> LENGTH: 30
 9737 <212> TYPE: DNA
 9738 <213> ORGANISM: unknown
 9740 <220> FEATURE:
 9741 <223> OTHER INFORMATION: unknown
 9743 <400> SEQUENCE: 46
 9744 cacacatcga tgggcaacgc cgatcagccg
 > 9747 160

Does Not Comply
 Corrected Diskette Needed

(p5.1-2)@

Pls explain
 source of
 genetic
 material.

Invalid
 Response

30

pls
 delete

↑ See item # 11
 on error summary
 sheet

<210> 44

<211> 7

<212> PPT

<213> unknown

Pls explain sourceOF genetic
material.

<220>

<223> (X) may be replaced by any amino acid

<220>

<221>

<222> (1) .. (7)

<223> unknown

<400> 44

His His Xaa Xaa Xaa Asp Gly

1

5

<210> 45

<211> 31

<212> DNA

<213> unknown

Same
error

<220>

<223> unknown

<400> 45

cacacagaat tcaccagcgc cactcgcgct t

See item
#11 on
error
summary
sheet.

31

FYI:

IF <213> response is
Artificial OR Unknown,
please explain source of
genetic material in section
<220> - <223>.

VERIFICATION SUMMARY

DATE: 02/15/2005

PATENT APPLICATION: US/09/976,059B

TIME: 07:48:05

Input Set : A:\3002-2US Sequ List AMENDED Dec 2004.ST25.txt

Output Set: N:\CRF4\02152005\I976059B.raw

2 M:271 C: Current Filing Date differs, Replaced Current Filing Date
713 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44
720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
747 M:254 E: No. of Bases conflict, this line has no nucleotides.